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1: NP_115972. ATP-binding cassette...[gi:21729873]

LOCUS ABCC11 1382 aa linear PRI 05-NOV-2002
DEFINITION ATP-binding cassette, sub-family C, member 11 isoform a; multi-resistance protein 8; ATP-binding cassette transporter MRP8; ATP-binding cassette protein C11 [Homo sapiens].

ACCESSION NP_115972
VERSION NP_115972.2 GI:21729873
DBSOURCE REFSEQ: accession NM_032583.2

KEYWORDS .

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (residues 1 to 1382)
AUTHORS Dean,M., Rzhetsky,A. and Allikmets,R.
TITLE The human ATP-binding cassette (ABC) transporter superfamily
JOURNAL Genome Res. 11 (7), 1156-1166 (2001)
MEDLINE 21329047
PUBMED 11435397

REFERENCE 2 (residues 1 to 1382)
AUTHORS Tammar,J., Prades,C., Arnould,I., Rzhetsky,A., Hutchinson,A., Adachi,M., Schuetz,J.D., Swoboda,K.J., Ptacek,L.J., Rosier,M., Dean,M. and Allikmets,R.
TITLE Two new genes from the human ATP-binding cassette transporter superfamily, ABCC11 and ABCC12, tandemly duplicated on chromosome 16q12
JOURNAL Gene 273 (1), 89-96 (2001)
MEDLINE 21376129
PUBMED 11483364

REFERENCE 3 (residues 1 to 1382)
AUTHORS Bera,T.K., Lee,S., Salvatore,G., Lee,B. and Pastan,I.
TITLE MRP8, a new member of ABC transporter superfamily, identified by EST database mining and gene prediction program, is highly expressed in breast cancer
JOURNAL Mol. Med. 7 (8), 509-516 (2001)
MEDLINE 21475973
PUBMED 11591886

REFERENCE 4 (residues 1 to 1382)
AUTHORS Yabuuchi,H., Shimizu,H., Takayanagi,S. and Ishikawa,T.
TITLE Multiple splicing variants of two new human ATP-binding cassette transporters, ABCC11 and ABCC12
JOURNAL Biochem. Biophys. Res. Commun. 288 (4), 933-939 (2001)
MEDLINE 21547789
PUBMED 11688999

COMMENT REVIEWED REFSEQ: This record has been curated by NCBI staff. The reference sequence was derived from AF367202.1. On Jul 11, 2002 this sequence version replaced gi:14211905. Summary: The protein encoded by this gene is a member of the

superfamily of ATP-binding cassette (ABC) transporters. ABC proteins transport various molecules across extra- and intra-cellular membranes. ABC genes are divided into seven distinct subfamilies (ABC1, MDR/TAP, MRP, ALD, OABP, GCN20, White). This ABC full transporter is a member of the MRP subfamily which is involved in multi-drug resistance. It is expressed at low levels in all tissues, except kidney, spleen, and colon. This gene and family member ABCC12 are determined to be derived by duplication and are both localized to chromosome 16q12.1. Their chromosomal localization, potential function, and expression patterns identify them as candidates for paroxysmal kinesigenic choreoathetosis, a disorder characterized by attacks of involuntary movements and postures, chorea, and dystonia. Multiple alternatively spliced transcript variants have been described for this gene.

Transcript Variant: This variant (1), as well as variant 2, encodes the predominant isoform (a).

FEATURES	Location/Qualifiers
<u>source</u>	1..1382 /organism="Homo sapiens" /db_xref="taxon:9606" /chromosome="16" /map="16q12.1"
<u>Protein</u>	1..1382 /product="ATP-binding cassette, sub-family C, member 11 isoform a" /note="multi-resistance protein 8; ATP-binding cassette transporter MRP8; ATP-binding cassette protein C11"
<u>Region</u>	163..427 /region_name="ABC transporter transmembrane region. This family represents a unit of six transmembrane helices. Many members of the ABC transporter family (pfam00005) have two such regions." /note="ABC_membrane" /db_xref="CDD:pfam00664"
<u>Region</u>	536..691 /region_name="ATPases associated with a variety of cellular activities" /note="AAA" /db_xref="CDD:smart00382"
<u>Region</u>	537..708 /region_name="ABC transporter. ABC transporters for a large family of proteins responsible for translocation of a variety of compounds across biological membranes. ABC transporters are the largest family of proteins in many completely sequenced bacteria. ABC transporters are composed of two copies of this domain and two copies of a transmembrane domain pfam00664. These four domains may belong to a single polypeptide or belong in different polypeptide chains" /note="ABC_tran" /db_xref="CDD:pfam00005"
<u>Region</u>	849..1094 /region_name="ABC transporter transmembrane region. This family represents a unit of six transmembrane helices. Many members of the ABC transporter family (pfam00005) have two such regions" /note="ABC_membrane" /db_xref="CDD:pfam00664"
<u>Region</u>	1168..1360 /region_name="ATPases associated with a variety of

Region

cellular activities"
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/note="ABC_tran"
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/note="transporter"
/db_xref="LocusID:85320"
/db_xref="MIM:607040"

CDS

ORIGIN

1 mtrkrtywvp nssgglnvrg idigddmvsg liykttytlqd gpwsqqernp eapgraavpp
61 wgkydaalrt mipfrpkprf papqpldnag lfsyltvswl tpmiqslrs rldentippl
121 svhdasdknv qrlhrlweee vsrrgiekas vllvmlrfqr trlifdallg icfciasvlg
181 piliipkile yseeqlgnvv hgvglcfalf lsecvklslf ssswiinqrt airfraavss
241 fafeklqfk svihitsgea isfftgdvny lfegvcygp vlitcaslvi csissyfiig
301 ytafiailcy llvfplavfm trmavkaqhh tsevsdqrir vtsevtcik likmytwekp
361 fakiiedlrr kerkllekcg lvqsltsitl fiiptvatav wvlihts1kl kltasmafsm
421 lasnllrls vffvpiavkg ltnsksavmr fkkfflqesp vfyyvqt1qdp skalvfeeat
481 lswqqtcpgi vngalelern ghasegmtrp rdalgpeeeeg nslgpelhki nlvvskgmmml
541 gvcgntgsgk ssllsailee mhllegsvgv qgslayvpqq awivsgnire nilmggaydk
601 arylqvlhcc slnrndllep fgdmtreiger glnlsggqkq rislaravys drqiyllddp
661 lsavdahvgk hifeecikk t lrgktvvlt hqqlqylefcg qillengki cengthselm
721 qkkgyaqli qkmhkeatsd mlqdakiae kpkesqala tsleeslgn avpehqltqe
781 eemeegslsw rvyhyiqaa ggymvscif ffvvlivflt ifsfwwlsyw leqgsgtnss
841 resngtmadl gniadnpqls fyqlvyglna llicvgvcs sgiftkvtrk astalhnklf
901 nkvfrcpmsf fdtipigrl1 ncfagdleql dqllpifseq flvlslmvia vllivsvlsp
961 yillmgaim vicfiyymmf kkaigvfkrl enyrsplfs hilnslqgls sihvygktd
1021 fisqfkrltd aqnnyllfl sstrwmalr eimtnlvsla valfvafgis stpysfkvma
1081 vnivlqllass fqatarigle teaqftaver ilqymkmcvs eaplhmeqts cpqgwpqhge
1141 iifqdhyhmky rdntptvlhg inltirghev vgivgrtgsg ksslgmalfr lvepmagril
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1261 skfpkklhtd vvenggnfsv gerqlliciar avlrnskiil ideatasidm etdtliqrti
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1381 lr

//
Revised: July 5, 2002.

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Oct 31 2002 16:00:17

FASTA searches a protein or DNA sequence data bank
version 3.3t05 March 30, 2000

Please cite:

W.R. Pearson & D.J. Lipman PNAS (1988) 85:2444-2448

/tmp.fastaCAACZaWfX: 1219 aa
>SEQ ID NO 23 human transporter
vs /tmp.fastaDAADZaWfX library
searching /tmp.fastaDAADZaWfX library

1382 residues in 1 sequences

FASTA (3.34 January 2000) function [optimized, BL50 matrix (15:-5)] ktup: 2
join: 40, opt: 28, gap-pen: -12/ -2, width: 16

Scan time: 0.050

The best scores are: opt

gi|21729873|ref|NP_115972.2| ATP-binding cassette (1382) 4838

>>gi|21729873|ref|NP_115972.2| ATP-binding cassette, sub (1382 aa)

initn: 7928 initl: 4838 opt: 4838

Smith-Waterman score: 7606; 88.061% identity in 1382 aa overlap (1-1219:1-1382)

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	70	80	90	100	110	120
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gi 217	WGKYDAALRTMIPFRPKPRFPAPQPLDNAGLFSYLTWSWLTPMIQSLRSRLDENTIPPL	70	80	90	100	110
	130	140	150	160	170	180
SEQ	SVHDASDKNVQLRHRLWEEEVSRRGIEKASVLLVMLRFQRTLIFDALLGICFCIASVLG	:::::::::::::::::::	:::::::::::::::::::	:::::::::::::::::::	:::::::::::::::::::	:::::::::::::::::::
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	190	200	210	220	230	240
SEQ	PILIIIPKILEYSEEQLGNVVHVGGLCFALFLSECVKSLSFSSSWIINQRTAIRFQAAVSS	:::::::::::::::::::	:::::::::::::::::::	:::::::::::::::::::	:::::::::::::::::::	:::::::::::::::::::
gi 217	PILIIIPKILEYSEEQLGNVVHVGGLCFALFLSECVKSLSFSSSWIINQRTAIRFRAAVSS	190	200	210	220	230
	250	260	270	280	290	300
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	310	320	330	340	350	360
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	370	380	390	400	410	420
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	LASLNLLRLSVFFVPIAVKGLTNSKSAVMRFKKFLQESPVFYVQTLQDPSKALVFEET					
SEQ	490	500	510	520	530	540
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gi 217	490	500	510	520	530	540
	LSWQQTCPGIVNGALELERNGHASEGMTRPRDALGPEEEGNSLGPELHKINLVSKGMML					
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gi 217	550	560	570	580	590	600
	GVCGNTGSGKSSLLSAILEEMHLLEGSVGQGSLAYVPQQAWIVSGNIRENILMGGAYDK					
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SEQ	980	990	1000	1010	1020	1030
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SEQ	1040	1050	1060	1070	1080	1090
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SEQ	1160	1170	1180	1190	1200	1210
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gi 217	LR					

1219 residues in 1 query sequences

1382 residues in 1 library sequences

Scomplib [version 3.3t05 March 30, 2000]

start: Mon Nov 11 10:23:05 2002 done: Mon Nov 11 10:23:06 2002

Scan time: 0.050 Display time: 2.400

Function used was FASTA